

Amendments to the Claims:

The following list of claims will replace all prior versions of the claims in the application:

1. (*Currently amended*) A method of ~~analyzing gene expression, gene annotation, and sample information in a relational format supporting~~ managing and retrieving biological data for efficient exploration and analysis, the method comprising:

providing a data warehouse which comprises three distinct databases comprising a gene expression database for storing quantitative gene expression measurements for tissues and cell lines ~~screened using various assays~~; a clinical database for storing ~~information~~ sample data on bio-samples and donors corresponding to the tissues and cell lines; and a fragment index database for storing information on biological properties for DNA fragments corresponding to the tissues and cell lines, wherein the data warehouse is arranged in a relational format;

providing a user interface for entry of a first query, wherein the first query comprises a first sample set or gene set for which additional information is sought, and wherein the sample set comprises a plurality of samples having one or more selected attributes and the gene set comprises at least one gene having one or more selected properties;

receiving a ~~the query regarding gene expression of one or more DNA fragments~~;

~~determining the level of gene expression of the one or more DNA fragments~~;

correlating ~~the level of gene expression~~ measurements within the gene expression database with the clinical database and the fragment index- first sample set or gene set of the first query; and

displaying at the user interface the results of said correlation correlated gene expression measurements responsive to the first query.

2. (*Original*) The method of claim 1, wherein the data warehouse is constructed in a star relational schema.

3. (*Original*) The method of claim 1, wherein the data warehouse is constructed in a snowflake relational schema.

4. (*Currently amended*) The method of claim 1, wherein the analysis of ~~gene expression, gene annotation, and sample information~~ further comprises identifying a gene signature analysis and the method further comprises analyzing the correlated gene expression measurements to identify two sets a present set of DNA fragments: those that are consistently expressed within the first sample set or gene set, and an absent set of DNA fragments those that are consistently not expressed within the first sample set or gene set.

5. (*Currently amended*) The method of claim 4, wherein the analysis of ~~gene expression, gene annotation, and sample information~~ further comprises a gene signature differential analysis and the method further comprises:

performing a gene signature analysis for a second sample set or gene set;
~~which compares~~ comparing the two different gene expression-signature analysis results;
and

~~derives~~ identifying four sets of DNA gene fragments comprising: those that are in both the first gene signature's present gene set and the second's absent gene set, those that are in both the first gene signature's absent gene set and the second's present gene set, those that are in both present gene sets, those that are in both absent gene sets

a present/absent gene set including fragments that are consistently expressed within the first sample set or gene set and consistently not expressed within the second sample set or gene set;

a present/present gene set including fragments that are consistently expressed within both the first and second sample set or gene set;

an absent/absent gene set including fragments that are consistently not expressed within both the first and second sample set or gene set; and

an absent/present gene set including fragments that are consistently not expressed within the first sample set or gene set and are consistently expressed within the second sample set or gene set.

6. (*Currently amended*) The method of claim 1, wherein the analysis of ~~gene expression, gene annotation, and sample information~~ further comprises a fold change analysis comprising:

calculating mean expression levels for each gene fragment within the first sample set or gene set;

before or after calculating mean expression levels for the first sample set or gene set, correlating gene expression measurements with a second query comprising a second sample set or gene set;

calculating mean expression levels of each gene fragment within the second sample set or gene set; and

which quantifies the comparing the mean expression levels for the two sample sets or gene sets to quantify a change in expression for differentially expressed genes between pairs of DNA fragments.

7. (*Currently amended*) The method of claim 1, wherein the analysis ~~of gene expression, gene annotation, and sample information~~ further comprises an E Northern analysis ~~which that~~ identifies DNA fragments with regard to a pair of user-selected percentiles over the values for a sample.

8. (*Currently amended*) A computer system comprising
a data warehouse which comprises three distinct databases comprising a gene expression database for storing quantitative gene expression measurements for tissues and cell lines screened using various assays; a clinical database for storing information sample data on bio-samples and donors corresponding to the tissues and cell lines; and a fragment index database for storing information on biological properties for DNA fragments corresponding to the tissues and cell lines, wherein the data warehouse is arranged in a relational format;

a data explorer for accessing and analyzing data in the data warehouse; and

a user interface capable of receiving a in communication with the data explorer for entering a first query regarding gene expression of one or more DNA fragments , wherein the first query comprises a first sample set or gene set for which additional information is sought, and wherein the sample set comprises a plurality of samples having one or more selected attributes and the gene set comprises at least one gene having one or more selected properties,

and for displaying the results of a correlation of the level of gene expression measurements with the clinical database and the fragment index first sample set or gene set.

9. *(Original)* The computer of claim 8, wherein the data warehouse is constructed in a star relational schema.

10. *(Original)* The computer of claim 8, wherein the data warehouse is constructed in a snowflake relational schema.

11. *(Currently amended)* The computer of claim 8, wherein the data explorer performs analysis of gene expression, gene annotation, and sample information further comprises identifying a gene signature analysis comprising analyzing the correlated gene expression measurements to identify two sets a present set of DNA fragments: those that are consistently expressed within the first sample set or gene set, and an absent set of DNA fragments those that are consistently not expressed within the first sample set or gene set.

12. *(Currently amended)* The computer of claim 8 11 , wherein the ~~analysis of gene expression, gene annotation, and sample information further comprises~~ data explorer performs a gene signature differential analysis comprising:

performing a gene signature analysis for a second sample set or gene set;

~~which compares~~ comparing the two different gene expression-signature analysis results;

and

~~derives identifying four sets of DNA gene fragments comprising: those that are in both the first gene signature's present gene set and the second's absent gene set, those that are in both the first gene signature's absent gene set and the second's present gene set, those that are in both present gene sets, those that are in both absent gene sets~~

a present/absent gene set including fragments that are consistently expressed within the first sample set or gene set and consistently not expressed within the second sample set or gene set;

a present/present gene set including fragments that are consistently expressed within both the first and second sample set or gene set;

an absent/absent gene set including fragments that are consistently not expressed within both the first and second sample set or gene set; and

an absent/present set including fragments that are consistently not expressed within the first sample set or gene set and are consistently expressed within the second sample set or gene set.

13. (*Currently amended*) The computer of claim 8, wherein the ~~analysis of gene expression, gene annotation, and sample information further comprises~~ data explorer performs a fold change analysis, comprising:

calculating mean expression levels for each gene fragment within the first sample set or gene set;

before or after calculating mean expression levels for the first sample set or gene set, correlating gene expression measurements with a second query comprising a second sample set or gene set;

calculating mean expression levels of each gene fragment within the second sample set or gene set; and

~~which quantifies the~~ comparing the mean expression levels for the two sample sets or gene sets to quantify a change in expression for differentially expressed genes between pairs of DNA fragments.

14. (*Currently amended*) The computer of claim 8, wherein the ~~analysis of gene expression, gene annotation, and sample information further comprises~~ data explorer performs an E Northern analysis which that identifies DNA fragments with regard to a pair of user-selected percentiles over the values for a sample.

15. (*Currently amended*) A computer program product comprising a computer-usable medium having computer-readable program code embodied thereon relating to a data warehouse comprising gene expression data and related information, which comprises a gene expression

~~database for storing quantitative gene expression measurements for tissues and cell lines screened using various assays; a clinical database for storing information on bio-samples and donors; and a fragment index for biological properties for DNA fragments;~~ the computer program product comprising computer-readable program code for effecting the following steps within a computing system:

arranging the data warehouse into three distinct databases comprising a gene expression database for storing quantitative gene expression measurements for tissues and cell lines, a clinical database for storing sample data on bio-samples and donors corresponding to the tissues and cell lines, and a fragment index database for storing information on biological properties for DNA fragments corresponding to the tissues and cell lines, wherein the data warehouse is arranged in a relational format;

providing an a user interface for receiving a query regarding gene expression of one or more DNA fragments entry of a first query, wherein the first query comprises a first sample set or gene set for which additional information is sought, and wherein the sample set comprises a plurality of samples having one or more selected attributes and the gene set comprises at least one gene having one or more selected properties;

~~determining the level of gene expression of the one or more DNA fragments;~~

correlating the level of gene expression with measurements within the gene expression database clinical database and the fragment S index with the sample set or gene set of the first query; and

displaying at the user interface the results of said correlation correlated gene expression measurements responsive to the first query.

16. (*Original*) The computer program product of claim 15, wherein the data warehouse is constructed in a star relational schema.

17. (*Original*) The computer program product of claim 15, wherein the data warehouse is constructed in a snowflake relational schema.

18. (*Currently amended*) The computer program product of claim 15, ~~wherein the analysis of gene expression, gene annotation, and sample information further comprises identifying~~ further comprising computer-readable program code for effecting a gene signature analysis comprising analyzing the correlated gene expression measurements to identify two sets a present set of DNA fragments: those that are consistently expressed within the first sample set or gene set, and an absent set of DNA fragments those that are consistently not expressed within the first sample set or gene set.

19. (*Currently amended*) The ~~method computer program product~~ of claim 15, ~~wherein the analysis of gene expression, gene annotation, and sample information further comprises 18,~~ further comprising computer-readable program code for effecting a gene signature differential analysis and the method further comprises:

performing a gene signature analysis for a second sample set or gene set;
~~which compares~~ comparing the two different gene expression-signature analysis results;
and

~~derives identifying~~ four sets of DNA gene fragments comprising: those that are in both the first gene signature's present gene set and the second's absent gene set, those that are in both the first gene signature's absent gene set and the second's present gene set, those that are in both present gene sets, those that are in both absent gene sets

a present/absent gene set including fragments that are consistently expressed within the first sample set or gene set and consistently not expressed within the second sample set or gene set;

a present/present gene set including fragments that are consistently expressed within both the first and second sample set or gene set;

an absent/absent gene set including fragments that are consistently not expressed within both the first and second sample set or gene set; and

an absent/present gene set including fragments that are consistently not expressed within the first sample set or gene set and are consistently expressed within the second sample set or gene set.

20. (*Currently amended*) The computer program product of claim 15, ~~wherein the analysis of gene expression, gene annotation, and sample information further comprises~~ further comprising computer-readable program code for effecting a fold change analysis comprising:

calculating mean expression levels for each gene fragment within the first sample set or gene set;

before or after calculating mean expression levels for the first sample set or gene set, correlating gene expression measurements with a second query comprising a second sample set or gene set;

calculating mean expression levels of each gene fragment within the second sample set or gene set; and

~~which quantifies the~~ comparing the mean expression levels for the two sample sets or gene sets to quantify a change in expression for differentially expressed genes between pairs of DNA fragments.

21. (*Currently amended*) The method of claim 15, ~~wherein the analysis of gene expression, gene annotation, and sample information further comprises~~ further comprising computer-readable program code for effecting an E Northern analysis which that identifies DNA fragments with regard to a pair of user-selected percentiles over the values for a sample.